

SEQUENCE LISTING AP20 Rec'd PCT/PTO 05 JUL 2006

<110> Avalon Pharmaceuticals

<120> Cancer-Linked Genes as Targets for Chemotherapy

<130> 689290-234

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<150> 60/534,419

<151> 2004-01-06

<160> 69

<170> PatentIn version 3.3

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&lt;212&gt; PRT

&lt;213&gt; Artificial

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&lt;210&gt; 9

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 20 25 30

Pro Thr Ala Glu Leu Ser Pro Pro Gly Ser Gly Lys Asp Pro Thr Glu  
 35 40 45

Ala Lys Ala Ala Pro Glu Gly Gln Val Arg Val Pro Phe Leu Glu Glu  
 50 55 60

Ala Gly Ala Arg Lys Ala Val Thr Leu Ala Leu Ala Thr Gly Phe Pro  
 65 70 75 80

Gly Ala Val Leu Ser Gln Glu Leu His Ser Ala Gly His Leu Gln Lys  
 85 90 95

Thr Val Phe Arg Val Tyr Phe Leu Leu Ser Ser Thr Gln Ser Pro Thr  
 100 105 110

Ala Ala Asn Ala Arg Gly Gln Lys Met Phe Gly Gly Arg Lys Thr Lys  
 115 120 125

Ala Gly Ser Gly Gly Gly Leu Thr Val Arg Val Cys Leu Gln Arg Arg  
 130 135 140

Glu Gly Ala Gly Ser Val Ser Ser Cys Phe Ser Lys Leu Gln Gly Pro  
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Gly Ser Pro Leu Gln Gly Arg Ala Pro Leu Leu Pro Ala Arg His Trp  
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Arg Trp Pro Pro Glu Arg Arg Arg Pro Thr Pro Ala Pro Gly Leu Ser  
 180 185 190

Gly Gly Asn Gly  
 195

&lt;210&gt; 12

&lt;211&gt; 1945

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&lt;213&gt; Artificial

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&lt;223&gt; cDNA or putative protein derived from a cDNA.

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Ser Glu Phe Gly Ala Pro Arg Trp Asn Asp Tyr Glu Val Pro Glu Glu  
35 40 45

Phe Asn Phe Ala Ser Tyr Val Leu Asp Tyr Trp Ala Gln Lys Glu Lys  
50 55 60

Glu Gly Lys Arg Gly Pro Asn Pro Ala Phe Trp Trp Val Asn Gly Gln  
65 70 75 80

Gly Asp Glu Val Lys Trp Ser Phe Arg Glu Met Gly Asp Leu Thr Arg  
85 90 95

Arg Val Ala Asn Val Phe Thr Gln Thr Cys Gly Leu Gln Gln Gly Asp  
100 105 110

His Leu Ala Leu Met Leu Pro Arg Val Pro Glu Trp Trp Leu Val Ala  
115 120 125

Val Gly Cys Met Arg Thr Gly Ile Ile Phe Ile Pro Ala Thr Ile Leu  
130 135 140

Leu Lys Ala Lys Asp Ile Leu Tyr Arg Leu Gln Leu Ser Lys Ala Lys  
145 150 155 160

Gly Ile Val Thr Ile Asp Ala Leu Ala Ser Glu Val Asp Ser Ile Ala  
165 170 175

Ser Gln Cys Pro Ser Leu Lys Thr Lys Leu Leu Val Ser Asp His Ser  
180 185 190

Arg Glu Gly Trp Leu Asp Phe Arg Ser Leu Val Lys Ser Ala Ser Pro  
195 200 205

Glu His Thr Cys Val Lys Ser Lys Thr Leu Asp Pro Met Val Ile Phe  
210 215 220

Phe Thr Ser Gly Thr Thr Gly Phe Pro Lys Met Ala Lys His Ser His  
225 230 235 240

Gly Leu Ala Leu Gln Pro Ser Phe Pro Gly Ser Arg Lys Leu Arg Ser  
245 250 255

Leu Lys Thr Ser Asp Val Ser Trp Cys Leu Ser Asp Ser Gly Trp Ile  
260 265 270

Val Ala Thr Ile Trp Thr Leu Val Glu Pro Trp Thr Ala Gly Cys Thr  
275 280 285

Val Phe Ile His His Leu Pro Gln Phe Asp Thr Lys Val Ile Ile Gln  
290 295 300

Thr Leu Leu Lys Tyr Pro Ile Asn His Phe Trp Gly Val Ser Ser Ile  
305 310 315 320

Tyr Arg Met Ile Leu Gln Gln Asp Phe Thr Ser Ile Arg Phe Pro Ala  
325 330 335

Leu Glu His Cys Tyr Thr Gly Gly Glu Val Val Leu Pro Lys Asp Gln  
340 345 350

Glu Glu Trp Lys Arg Arg Thr Gly Leu Leu Leu Tyr Glu Asn Tyr Gly  
355 360 365

Gln Ser Glu Thr Gly Leu Ile Cys Ala Thr Tyr Trp Gly Met Lys Ile  
370 375 380

Lys Pro Gly Phe Met Gly Lys Ala Thr Pro Pro Tyr Asp Val Gln Val  
385 390 395 400

Ile Asp Asp Lys Gly Ser Ile Leu Pro Pro Asn Thr Glu Gly Asn Ile  
405 410 415

Gly Ile Arg Ile Lys Pro Val Arg Pro Val Ser Leu Phe Met Cys Tyr  
420 425 430

Glu Gly Asp Pro Glu Lys Thr Ala Lys Val Glu Cys Gly Asp Phe Tyr  
435 440 445

Asn Thr Gly Asp Arg Gly Lys Met Asp Glu Glu Gly Tyr Ile Cys Phe  
450 455 460

Leu Gly Arg Ser Asp Asp Ile Ile Asn Ala Ser Gly Tyr Arg Ile Gly  
465 470 475 480

Pro Ala Glu Val Glu Ser Ala Leu Val Glu His Pro Ala Val Ala Glu  
485 490 495

Ser Ala Val Val Gly Ser Pro Asp Pro Ile Arg Gly Glu Val Val Lys  
500 505 510

Ala Phe Ile Val Leu Thr Pro Gln Phe Leu Ser His Asp Lys Asp Gln  
515 520 525

Leu Thr Lys Glu Leu Gln Gln His Val Lys Ser Val Thr Ala Pro Tyr  
530 535 540

Lys Tyr Pro Arg Asn Val Glu Phe Val Ser Glu Leu Pro Lys Thr Ile  
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Thr Gly Lys Ile Glu Arg Lys Glu Leu Arg Lys Lys Glu Thr Gly Gln  
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&lt;210&gt; 15

&lt;211&gt; 795

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; cDNA or putative protein derived from a cDNA.

&lt;400&gt; 15

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Leu Ala Ile Leu Leu Leu Leu Trp Glu Ala Gly Ser Glu Ala Val Arg
20              25              30

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Tyr Ser Ile Pro Glu Glu Thr Glu Ser Gly Tyr Ser Val Ala Asn Leu
35              40              45

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Ala Lys Asp Leu Gly Leu Gly Val Gly Glu Leu Ala Thr Arg Gly Ala
50              55              60

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Arg Met His Tyr Lys Gly Asn Lys Glu Leu Leu Gln Leu Asp Ile Lys
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Thr Gly Asn Leu Leu Leu Tyr Glu Lys Leu Asp Arg Glu Val Met Cys
85              90              95

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Gly Ala Thr Glu Pro Cys Ile Leu His Phe Gln Leu Leu Leu Glu Asn
100             105             110

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Pro Val Gln Phe Phe Gln Thr Asp Leu Gln Leu Thr Asp Ile Asn Asp
115             120             125

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His Ala Pro Glu Phe Pro Glu Lys Glu Met Leu Leu Lys Ile Pro Glu
130             135             140

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Ser Thr Gln Pro Gly Thr Val Phe Pro Leu Lys Ile Ala Gln Asp Phe
145             150             155             160

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Asp Ile Gly Ser Asn Thr Val Gln Asn Tyr Thr Ile Ser Pro Asn Ser

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Ser Leu Thr Leu Thr Ala Leu Asp Gly Gly Ala Pro Pro Arg Ser Gly	210		215		220	
Thr Thr Thr Ile Arg Ile Val Val Leu Asp Asn Asn Asp Asn Ala Pro	225		230		235	240
Glu Phe Leu Gln Ser Phe Tyr Glu Val Gln Val Pro Glu Asn Ser Pro		245		250		255
Leu Asn Ser Leu Val Val Val Val Ser Ala Arg Asp Leu Asp Ala Gly		260		265		270
Ala Tyr Gly Ser Val Ala Tyr Ala Leu Phe Gln Gly Asp Glu Val Thr		275		280		285
Gln Pro Phe Val Ile Asp Glu Lys Thr Ala Glu Ile Arg Leu Lys Arg		290		295		300
Ala Leu Asp Phe Glu Ala Thr Pro Tyr Tyr Asn Val Glu Ile Val Ala	305		310		315	320
Thr Asp Gly Gly Gly Leu Ser Gly Lys Cys Thr Val Ala Ile Glu Val		325		330		335
Val Asp Val Asn Asp Asn Ala Pro Glu Leu Thr Met Ser Thr Leu Ser		340		345		350
Ser Pro Thr Pro Glu Asn Ala Pro Glu Thr Val Val Ala Val Phe Ser		355		360		365
Val Ser Asp Pro Asp Ser Gly Asp Asn Gly Arg Met Ile Cys Ser Ile		370		375		380
Gln Asn Asp Leu Pro Phe Leu Leu Lys Pro Thr Leu Lys Asn Phe Tyr	385		390		395	400
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Asn Ile Thr Ile Thr Val Thr Asp Met Gly Thr Pro Arg Leu Lys Thr  
420 425 430

Glu His Asn Ile Thr Val Leu Val Ser Asp Val Asn Asp Asn Ala Pro  
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Ala Phe Thr Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser  
450 455 460

Pro Ala Leu His Ile Gly Ser Val Ser Ala Thr Asp Arg Asp Ser Gly  
465 470 475 480

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Leu Arg Leu Ala Ser Leu Val Ser Ile Asn Ala Asp Asn Gly His Leu  
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Phe Ala Leu Arg Ser Leu Asp Tyr Glu Ala Leu Gln Ala Phe Glu Phe  
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530 535 540

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545 550 555 560

Leu Tyr Pro Leu Gln Asn Gly Ser Ala Pro Cys Thr Glu Leu Val Pro  
565 570 575

Arg Ala Ala Glu Pro Gly Tyr Leu Val Thr Lys Val Val Ala Val Asp  
580 585 590

Gly Asp Ser Gly Gln Asn Ala Trp Leu Ser Tyr Gln Leu Leu Lys Ala  
595 600 605

Thr Glu Pro Gly Leu Phe Ser Met Trp Ala His Asn Gly Glu Val Arg  
610 615 620

Thr Ala Arg Leu Leu Ser Glu Arg Asp Ala Ala Lys His Arg Leu Val  
625 630 635 640

Val Leu Val Lys Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala Thr  
645 650 655



Leu His Val Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu  
660 665 670

Pro Glu Ala Ala Pro Ala Gln Ala Gln Ala Asp Ser Leu Thr Val Tyr  
675 680 685

Leu Val Val Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Phe Ser Val  
690 695 700

Leu Leu Phe Val Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala Ser  
705 710 715 720

Val Gly Arg Cys Ser Val Pro Glu Gly Pro Phe Pro Gly His Leu Val  
725 730 735

Asp Val Ser Gly Thr Gly Thr Leu Ser Gln Ser Tyr His Tyr Glu Val  
740 745 750

Cys Leu Thr Gly Asp Ser Gly Ala Gly Glu Phe Lys Phe Leu Lys Pro  
755 760 765

Ile Ile Pro Asn Leu Leu Pro Gln Gly Ala Gly Glu Glu Ile Gly Lys  
770 775 780

Thr Ala Ala Phe Arg Asn Ser Phe Gly Leu Asn  
785 790 795

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<223> cDNA or putative protein derived from a cDNA.

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aaccactgca ctgacctgcc tttatgaaca ctgtgttcat aaagttgatg ttactgaaa 180  
cttccttaat tccctgagtg tgctgccct ttagttgcc acctatgaga taggtagga 240  
ctatcattaa tttccatttt acagatgagg gaagtggggg ttagacaggg taacaaattt 300  
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<220>  
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 agaccagggc agaatgcac tcttcctttc tcttggtttt cctggataag gactgcatca 180  
 ttcctgtgga aggacaggcc atcagctccg aaacactgta tgtattttcc agtatatact 240  
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 taaaatggaa ataatgatag tacctaccta tctcataggt ggcaactaca aggggcagca 360  
 cactcagggg attaaggaag tttcagtga catcaacttt atgaacacag tgttcataaa 420  
 ggcaggtcag tgcagtgtt tgggagccag gagaagcacg tgggccggag tgtgcctgca 480  
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<210> 18  
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<400> 18

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 20 25 30

Lys Ser Gly Lys Lys Thr Glu Lys Thr Arg Ala Glu Cys Ile Ser Ser  
 35 40 45

Phe Leu Leu Ala Phe Leu Asp Lys Asp Cys Ile Ile Pro Val Glu Gly  
 50 55 60

Gln Ala Ile Ser Ser Glu Thr Leu Tyr Val Phe Ser Ser Ile Tyr Cys  
 65 70 75 80

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 cagtgcagtg gtttgggagc caggagaagc acgtgggccg gagtgtgcct gcaggagaca 240  
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 <211> 832

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<220>  
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<220>  
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<223> n is a, c, g, or t

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ccaaaaacat aaatgctact ttactatcaa ttgaagcata ttatttcaat tattctggtt 660  
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cagangtaaa gtgctatcaa ttactattta agagttctat ttttgaaaaa gtgagaatta 780  
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<210> 21  
<211> 2367  
<212> DNA  
<213> Artificial

<220>  
<223> cDNA or putative protein derived from a cDNA.

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gatgtctggg ctgctgtaca agggagtccc ctttcagggtg tgggtgctaga catggctact 360  
cctgctggat gtctaggtgg tagaaaccaa ggacctaggg aaataaccagg tacagccttt 420  
ccatgctcat ccagagcagg acaaacaggc caggcgtgtg caggagccca ggtctccagc 480  
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 <212> PRT  
 <213> Artificial

<220>  
 <223> cDNA or putative protein derived from a cDNA.

<400> 22

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Glu Ile Pro Gly Thr Ala Phe Pro Cys Ser Ser Arg Ala Gly Gln Thr
20           25           30

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Gly Gln Ala Val Ser Gly Ala Gln Val Ser Ser Trp Arg Glu Arg Gln
35           40           45

```

```

Pro Phe Gly Gly Ser Arg Gly Pro Leu His Ile Leu Gly Thr Asp Gly
50           55           60

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Asn Val Asp Thr Thr Gly Lys Leu Gly Leu Val Pro Thr Pro Pro Arg
65           70           75           80

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Ile Gln Lys Glu Thr Lys Gln Gly Ala Leu Cys Gly Met Lys Pro Pro
85           90           95

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Phe Leu Pro Glu Ala Leu Leu Thr Val Trp Trp Leu Pro Phe Val Ala
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Val Ser Leu Cys Leu Phe
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<210> 23

&lt;211&gt; 3067

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; cDNA or putative protein derived from a cDNA.

&lt;400&gt; 23

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<400> 24

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Ser Phe Glu Asp Val Ala Val Gly Phe Thr Arg Glu Glu Trp Gln Phe  
20 25 30

Leu Asp Gln Ser Gln Lys Val Leu Tyr Lys Glu Val Met Leu Glu Asn  
35 40 45

Tyr Ile Asn Leu Val Ser Ile Gly Tyr Arg Gly Thr Lys Pro Asp Ser  
50 55 60

Leu Phe Lys Leu Glu Gln Gly Glu Pro Pro Gly Ile Val Glu Gly Ala  
65 70 75 80

Ala His Ser Gln Ile Cys Pro Gly Phe Val Ile Gln Ser Arg Arg Tyr  
85 90 95

Ala Gly Lys Asp Ser Asp Ala Phe Gly Gly Tyr Gly Arg Ser Cys Leu  
100 105 110

His Ile Lys Cys Asp Lys Thr Leu Thr Gly Val Lys Tyr His Arg Cys  
115 120 125

Val Lys Pro Ser Ser Pro Lys Ser Gln Leu Asn Asp Leu Gln Lys Ile  
130 135 140

Cys Ala Gly Gly Lys Pro His Glu Cys Ser Val Cys Gly Arg Ala Phe  
145 150 155 160

Ser Arg Lys Ala Gln Leu Ile Gln His Gln Arg Thr Glu Arg Gly Glu  
165 170 175

Lys Pro His Gly Cys Gly Glu Cys Gly Lys Thr Phe Met Arg Lys Ile  
180 185 190

Gln Leu Thr Glu His Gln Arg Thr His Thr Gly Glu Lys Pro His Glu  
195 200 205

Cys Ser Glu Cys Gly Lys Ala Phe Ser Arg Lys Ser Gln Leu Met Val  
210 215 220

His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Arg Cys Ser Glu Cys  
225 230 235 240

Gly Lys Ala Phe Ser Arg Lys Cys Arg Leu Asn Arg His Gln Arg Ser  
245 250 255

His Thr Gly Glu Lys Leu Tyr Gly Cys Ser Val Cys Gly Lys Ala Phe  
260 265 270

Ser Gln Lys Ala Tyr Leu Thr Ala His Gln Arg Leu His Thr Gly Asp  
275 280 285

Lys Pro Tyr Lys Cys Ser Asp Cys Gly Arg Thr Phe Tyr Phe Lys Ser  
290 295 300

Asp Leu Thr Arg His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu  
305 310 315 320

Cys Ser Glu Cys Glu Lys Ala Phe Arg Ser Lys Ser Lys Leu Ile Gln  
325 330 335

His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Ser Cys Arg Glu Cys  
340 345 350

Gly Lys Ala Phe Ala His Met Ser Val Leu Ile Lys His Glu Lys Thr  
355 360 365

His Ile Arg Glu Thr Ala Ile Asn Ser Leu Thr Val Glu Lys Pro Ser  
370 375 380

Ser Arg Ser His Thr Ser Leu Tyr Met Ser Glu Leu Ile Gln Glu Gln  
385 390 395 400

Lys Thr Val Asn Thr Val Pro Ile Glu Met Pro Ser Ser Gly Thr Pro  
405 410 415

Pro Leu Leu Asn Lys Ser Glu Arg Leu Val Gly Arg Asn Val Val Ile  
420 425 430

Val Glu Gln Pro Phe Pro Arg Asn Gln Ala Phe Val Val Asn Gln Glu  
435 440 445

Phe Glu Gln Arg Ile Ser Leu Thr Asn Glu Val Asn Val Ala Pro Ser  
 450 455 460

Val Ile Asn Tyr Ile Leu Tyr Leu Thr Asp Ile Val Ser Glu  
 465 470 475

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 <212> DNA  
 <213> Artificial

<220>  
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<210> 27



<211> 156  
 <212> PRT  
 <213> Artificial

<220>  
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<400> 27

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Gly Phe Leu Leu Gly Leu Asp Pro Leu Leu Ala Lys Leu Leu Ser Met  
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Gln Gln Ala Arg Glu Thr Ala Val Gln Gln Tyr Lys Lys Leu Glu Glu  
 35 40 45

Glu Ile Gln Thr Leu Arg Val Tyr Tyr Ser Leu His Lys Ser Leu Ser  
 50 55 60

Gln Glu Glu Asn Leu Lys Asp Gln Phe Asn Tyr Thr Leu Ser Thr Tyr  
 65 70 75 80

Glu Glu Ala Leu Lys Asn Arg Glu Asn Ile Val Ser Ile Thr Gln Gln  
 85 90 95

Gln Asn Glu Glu Leu Ala Thr Gln Leu Gln Gln Ala Leu Thr Glu Arg  
 100 105 110

Ala Asn Met Glu Leu Gln Leu Gln His Ala Arg Glu Ala Ser Gln Val  
 115 120 125

Ala Asn Glu Lys Val Gln Lys Leu Glu Arg Leu Val Asp Val Leu Arg  
 130 135 140

Lys Lys Val Gly Thr Gly Thr Met Arg Thr Val Ile  
 145 150 155

<210> 28  
 <211> 2643  
 <212> DNA  
 <213> Artificial

<220>  
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&lt;210&gt; 29

&lt;211&gt; 442

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; cDNA or putative protein derived from a cDNA.

&lt;400&gt; 29

```

Met Glu Asn Trp Ser Lys Asp Ile Thr His Ser Tyr Leu Glu Gln Glu
1             5             10             15

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```

Thr Thr Gly Ile Asn Lys Ser Thr Gln Pro Asp Glu Gln Leu Thr Met
20             25             30

```

Asn Ser Glu Lys Ser Met His Arg Lys Ser Thr Glu Leu Val Asn Glu  
 35 40 45

Ile Thr Cys Glu Asn Thr Glu Trp Pro Gly Gln Arg Ser Thr Asn Phe  
 50 55 60

Gln Ile Ile Ser Ser Tyr Pro Asp Asp Glu Ser Val Tyr Cys Thr Thr  
 65 70 75 80

Glu Lys Tyr Asn Val Met Glu His Arg His Asn Asp Met His Tyr Glu  
 85 90 95

Cys Met Thr Pro Cys Gln Val Thr Ser Asp Ser Asp Lys Glu Lys Thr  
 100 105 110

Ile Ala Phe Leu Leu Lys Glu Leu Asp Ile Leu Arg Thr Ser Asn Lys  
 115 120 125

Lys Leu Gln Gln Lys Leu Ala Lys Glu Asp Lys Glu Gln Arg Lys Leu  
 130 135 140

Lys Phe Lys Leu Glu Leu Gln Glu Lys Glu Thr Glu Ala Lys Ile Ala  
 145 150 155 160

Glu Lys Thr Ala Ala Leu Val Glu Glu Val Tyr Phe Ala Gln Lys Glu  
 165 170 175

Arg Asp Glu Ala Val Met Ser Arg Leu Gln Leu Ala Ile Glu Glu Arg  
 180 185 190

Asp Glu Ala Ile Ala Arg Ala Lys His Met Glu Met Ser Leu Lys Val  
 195 200 205

Leu Glu Asn Ile Asn Pro Glu Glu Asn Asp Met Thr Leu Gln Glu Leu  
 210 215 220

Leu Asn Arg Ile Asn Asn Ala Asp Thr Gly Ile Ala Ile Gln Lys Asn  
 225 230 235 240

Gly Ala Ile Ile Val Asp Arg Ile Tyr Lys Thr Lys Glu Cys Lys Met  
 245 250 255

Arg Ile Thr Ala Glu Glu Met Ser Ala Leu Ile Glu Glu Arg Asp Ala  
 260 265 270

Ala Leu Ser Lys Cys Lys Arg Leu Glu Gln Glu Leu His His Val Lys  
 275 280 285

Glu Gln Asn Gln Thr Ser Ala Asn Asn Met Arg His Leu Thr Ala Glu  
 290 295 300

Asn Asn Gln Glu Arg Ala Leu Lys Ala Lys Leu Leu Ser Met Gln Gln  
 305 310 315 320

Ala Arg Glu Thr Ala Val Gln Gln Tyr Lys Lys Leu Glu Glu Glu Ile  
 325 330 335

Gln Thr Leu Arg Val Tyr Tyr Ser Leu His Lys Ser Leu Ser Gln Glu  
 340 345 350

Glu Asn Leu Lys Asp Gln Phe Asn Tyr Thr Leu Ser Thr Tyr Glu Glu  
 355 360 365

Ala Leu Lys Asn Arg Glu Asn Ile Val Ser Ile Thr Gln Gln Gln Asn  
 370 375 380

Glu Glu Leu Ala Thr Gln Leu Gln Gln Ala Leu Thr Glu Arg Ala Asn  
 385 390 395 400

Met Glu Leu Gln Leu Gln His Ala Arg Glu Ala Ser Gln Val Ala Asn  
 405 410 415

Glu Lys Val Gln Lys Leu Glu Arg Leu Val Asp Val Leu Arg Lys Lys  
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Val Gly Thr Gly Thr Met Arg Thr Val Ile  
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 <213> Artificial

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 gcagaaggaa cgtgatgaag ctgttatgtc tagactgcaa ttagccattg aggagagaga 240  
 tgaagcaatt gcacgagcca agcatatgga aatgtctcta aaagtgtctag aaaatattaa 300  
 ccctgaagaa aatgacatga cattacagga attactgaac agaataaaca atgcagacac 360  
 agggatagct attcagaaga atggagctat aattgtggat agaatctaca agaccaagga 420  
 atgtaaaatg agaataactg cagaagaaat gagtgcacta atagaagaac gggatgtctgc 480

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aatttgttta ataagagatg gatataatga aattacattc atcaaggcat gatttttgtt 1620
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<210> 31  
 <211> 261  
 <212> PRT  
 <213> Artificial

<220>  
 <223> cDNA or putative protein derived from a cDNA.

<400> 31

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Met Ser Arg Leu Gln Leu Ala Ile Glu Glu Arg Asp Glu Ala Ile Ala
1           5           10          15

```

```

Arg Ala Lys His Met Glu Met Ser Leu Lys Val Leu Glu Asn Ile Asn
          20          25          30

```

```

Pro Glu Glu Asn Asp Met Thr Leu Gln Glu Leu Leu Asn Arg Ile Asn
          35          40          45

```

```

Asn Ala Asp Thr Gly Ile Ala Ile Gln Lys Asn Gly Ala Ile Ile Val
50          55          60

```

```

Asp Arg Ile Tyr Lys Thr Lys Glu Cys Lys Met Arg Ile Thr Ala Glu
65          70          75          80

```

```

Glu Met Ser Ala Leu Ile Glu Glu Arg Asp Ala Ala Leu Ser Lys Cys
          85          90          95

```

```

Lys Arg Leu Glu Gln Glu Leu His His Val Lys Glu Gln Asn Gln Thr
          100         105         110

```

Ser Ala Asn Asn Met Arg His Leu Thr Ala Glu Asn Asn Gln Glu Arg  
 115 120 125

Ala Leu Lys Ala Lys Leu Leu Ser Met Gln Gln Ala Arg Glu Thr Ala  
 130 135 140

Val Gln Gln Tyr Lys Lys Leu Glu Glu Glu Ile Gln Thr Leu Arg Val  
 145 150 155 160

Tyr Tyr Ser Leu His Lys Ser Leu Ser Gln Glu Glu Asn Leu Lys Asp  
 165 170 175

Gln Phe Asn Tyr Thr Leu Ser Thr Tyr Glu Glu Ala Leu Lys Asn Arg  
 180 185 190

Glu Asn Ile Val Ser Ile Thr Gln Gln Gln Asn Glu Glu Leu Ala Thr  
 195 200 205

Gln Leu Gln Gln Ala Leu Thr Glu Arg Ala Asn Met Glu Leu Gln Leu  
 210 215 220

Gln His Ala Arg Glu Ala Ser Gln Val Ala Asn Glu Lys Val Gln Lys  
 225 230 235 240

Leu Glu Arg Leu Val Asp Val Leu Arg Lys Lys Val Gly Thr Gly Thr  
 245 250 255

Met Arg Thr Val Ile  
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 <211> 2452  
 <212> DNA  
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<210> 33  
 <211> 411  
 <212> PRT  
 <213> Artificial

<220>  
 <223> cDNA or putative protein derived from a cDNA.

<400> 33

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Met Asn Ser Glu Lys Ser Met His Arg Lys Ser Thr Glu Leu Val Asn
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Glu Ile Thr Cys Glu Asn Thr Glu Trp Pro Gly Gln Arg Ser Thr Asn
          20           25           30

```

```

Phe Gln Ile Ile Ser Ser Tyr Pro Asp Asp Glu Ser Val Tyr Cys Thr
          35           40           45

```

```

Thr Glu Lys Tyr Asn Val Met Glu His Arg His Asn Asp Met His Tyr
          50           55           60

```

```

Glu Cys Met Thr Pro Cys Gln Val Thr Ser Asp Ser Asp Lys Glu Lys
65           70           75           80

```

Thr Ile Ala Phe Leu Leu Lys Glu Leu Asp Ile Leu Arg Thr Ser Asn  
85 90 95

Lys Lys Leu Gln Gln Lys Leu Ala Lys Glu Asp Lys Glu Gln Arg Lys  
100 105 110

Leu Lys Phe Lys Leu Glu Leu Gln Glu Lys Glu Thr Glu Ala Lys Ile  
115 120 125

Ala Glu Lys Thr Ala Ala Leu Val Glu Glu Val Tyr Phe Ala Gln Lys  
130 135 140

Glu Arg Asp Glu Ala Val Met Ser Arg Leu Gln Leu Ala Ile Glu Glu  
145 150 155 160

Arg Asp Glu Ala Ile Ala Arg Ala Lys His Met Glu Met Ser Leu Lys  
165 170 175

Val Leu Glu Asn Ile Asn Pro Glu Glu Asn Asp Met Thr Leu Gln Glu  
180 185 190

Leu Leu Asn Arg Ile Asn Asn Ala Asp Thr Gly Ile Ala Ile Gln Lys  
195 200 205

Asn Gly Ala Ile Ile Val Asp Arg Ile Tyr Lys Thr Lys Glu Cys Lys  
210 215 220

Met Arg Ile Thr Ala Glu Glu Met Ser Ala Leu Ile Glu Glu Arg Asp  
225 230 235 240

Ala Ala Leu Ser Lys Cys Lys Arg Leu Glu Gln Glu Leu His His Val  
245 250 255

Lys Glu Gln Asn Gln Thr Ser Ala Asn Asn Met Arg His Leu Thr Ala  
260 265 270

Glu Asn Asn Gln Glu Arg Ala Leu Lys Ala Lys Leu Leu Ser Met Gln  
275 280 285

Gln Ala Arg Glu Thr Ala Val Gln Gln Tyr Lys Lys Leu Glu Glu Glu  
290 295 300

Ile Gln Thr Leu Arg Val Tyr Tyr Ser Leu His Lys Ser Leu Ser Gln  
305 310 315 320

Glu Glu Asn Leu Lys Asp Gln Phe Asn Tyr Thr Leu Ser Thr Tyr Glu



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&lt;210&gt; 35

&lt;211&gt; 442

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; cDNA or putative protein derived from a cDNA.

&lt;400&gt; 35

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Met Glu Asn Trp Ser Lys Asp Ile Thr His Ser Tyr Leu Glu Gln Glu
1           5           10           15

```

```

Thr Thr Gly Ile Asn Lys Ser Thr Gln Pro Asp Glu Gln Leu Thr Met
          20           25           30

```

```

Asn Ser Glu Lys Ser Met His Arg Lys Ser Thr Glu Leu Val Asn Glu
          35           40           45

```

```

Ile Thr Cys Glu Asn Thr Glu Trp Pro Gly Gln Arg Ser Thr Asn Phe
50           55           60

```

```

Gln Ile Ile Ser Ser Tyr Pro Asp Asp Glu Ser Val Tyr Cys Thr Thr
65           70           75           80

```

```

Glu Lys Tyr Asn Val Met Glu His Arg His Asn Asp Met His Tyr Glu
          85           90           95

```

```

Cys Met Thr Pro Cys Gln Val Thr Ser Asp Ser Asp Lys Glu Lys Thr
          100          105          110

```

```

Ile Ala Phe Leu Leu Lys Glu Leu Asp Ile Leu Arg Thr Ser Asn Lys
          115          120          125

```

```

Lys Leu Gln Gln Lys Leu Ala Lys Glu Asp Lys Glu Gln Arg Lys Leu
          130          135          140

```

```

Lys Phe Lys Leu Glu Leu Gln Glu Lys Glu Thr Glu Ala Lys Ile Ala
          145          150          155          160

```

Glu Lys Thr Ala Ala Leu Val Glu Glu Val Tyr Phe Ala Gln Lys Glu  
 165 170 175

Arg Asp Glu Ala Val Met Ser Arg Leu Gln Leu Ala Ile Glu Glu Arg  
 180 185 190

Asp Glu Ala Ile Ala Arg Ala Lys His Met Glu Met Ser Leu Lys Val  
 195 200 205

Leu Glu Asn Ile Asn Pro Glu Glu Asn Asp Met Thr Leu Gln Glu Leu  
 210 215 220

Leu Asn Arg Ile Asn Asn Ala Asp Thr Gly Ile Ala Ile Gln Lys Asn  
 225 230 235 240

Gly Ala Ile Ile Val Asp Arg Ile Tyr Lys Thr Lys Glu Cys Lys Met  
 245 250 255

Arg Ile Thr Ala Glu Glu Met Ser Ala Leu Ile Glu Glu Arg Asp Ala  
 260 265 270

Ala Leu Ser Lys Cys Lys Arg Leu Glu Gln Glu Leu His His Val Lys  
 275 280 285

Glu Gln Asn Gln Thr Ser Ala Asn Asn Met Arg His Leu Thr Ala Glu  
 290 295 300

Asn Asn Gln Glu Arg Ala Leu Lys Ala Lys Leu Leu Ser Met Gln Gln  
 305 310 315 320

Ala Arg Glu Thr Ala Val Gln Gln Tyr Lys Lys Leu Glu Glu Glu Ile  
 325 330 335

Gln Thr Leu Arg Val Tyr Tyr Ser Leu His Lys Ser Leu Ser Gln Glu  
 340 345 350

Glu Asn Leu Lys Asp Gln Phe Asn Tyr Thr Leu Ser Thr Tyr Glu Glu  
 355 360 365

Ala Leu Lys Asn Arg Glu Asn Ile Val Ser Ile Thr Gln Gln Gln Asn  
 370 375 380

Glu Glu Leu Ala Thr Gln Leu Gln Gln Ala Leu Thr Glu Arg Ala Asn  
 385 390 395 400

Met Glu Leu Gln Leu Gln His Ala Arg Glu Ala Ser Gln Val Ala Asn  
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Glu Lys Val Gln Lys Leu Glu Arg Leu Val Asp Val Leu Arg Lys Lys  
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Val Gly Thr Gly Thr Met Arg Thr Val Ile  
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Gly Gly Arg Gly Asn Lys Phe Ala Gln Met Arg Tyr Ser Leu Arg Leu  
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Leu Arg Ala Met Val Tyr Leu Glu Asp Glu Thr Val Asn Lys Asp Leu  
 50 55 60

Cys Glu Lys Gly Thr Ile Gln Gln Met Ile Gly Ile Phe Lys Asn Ile  
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Ile Ser Lys Pro Asn Glu Lys Glu Glu Ala Ile Val Leu Glu Ile Gln  
 85 90 95

Ser Asp Ile Leu Leu Ile Leu Ser Gly Leu Cys Glu Asn His Ile Gln  
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Arg Lys Glu Ile Phe Gly Thr Glu Gly Val Asp Ile Val Leu His Val  
 115 120 125

Met Lys Thr Asp Pro Arg Lys Leu Gln Ser Gly Leu Gly Tyr Asn Val  
 130 135 140

Leu Leu Phe Ser Thr Leu Asp Ser Ile Trp Cys Cys Ile Leu Gly Cys  
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Tyr Pro Ser Glu Asp Tyr Phe Leu Glu Lys Glu Gly Ile Phe Leu Leu  
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Leu Asp Leu Leu Ala Leu Asn Gln Lys Lys Phe Cys Asn Leu Ile Leu  
 180 185 190

Gly Ile Met Val Glu Phe Cys Asp Asn Pro Lys Thr Ala Ala His Val  
 195 200 205

Asn Ala Trp Gln Gly Lys Lys Asp Gln Thr Ala Ala Ser Leu Leu Ile

210 215 220

Lys Leu Trp Arg Lys Glu Glu Lys Glu Leu Gly Val Lys Arg Asp Lys  
225 230 235 240

Asn Gly Lys Ile Ile Asp Phe Glu Asn Leu Pro Gly Leu Ser Ala Glu  
245 250 255

Asp Phe Val Thr Leu Cys Ile Ile His Arg Tyr Leu Asp Phe Lys Ile  
260 265 270

Gly Glu Ile Trp Asn Glu Ile Tyr Glu Glu Ile Lys Leu Glu Lys Leu  
275 280 285

Arg Pro Val Thr Thr Asp Lys Lys Ala Leu Glu Ala Ile Thr Thr Ala  
290 295 300

Ser Glu Asn Ile Gly Lys Met Val Ala Ser Leu Gln Ser Asp Ile Ile  
305 310 315 320

Glu Ser Gln Ala Cys Gln Asp Met Gln Asn Glu Gln Lys Val Tyr Ala  
325 330 335

Lys Ile Gln Ala Thr His Lys Gln Arg Glu Leu Ala Asn Lys Ser Trp  
340 345 350

Glu Asp Phe Leu Ala Arg Thr Ser Asn Ala Lys Thr Leu Lys Lys Ala  
355 360 365

Lys Arg Leu Gln Glu Lys Ala Ile Glu Ala Ser Arg Tyr His Lys Arg  
370 375 380

Pro Gln Asn Ala Ile Phe His Gln Thr His Ile Lys Gly Leu Asn Thr  
385 390 395 400

Met Val Pro Ser Gly Gly Val Val Thr Val Glu Ser Thr Pro Ala Arg  
405 410 415

Leu Val Gly Gly Pro Leu Val Asp Thr Asp Ile Ala Leu Lys Lys Leu  
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Thr Ile Met Met Lys Ala Gln Ala Ala Ser Gly Ile Cys Thr His Leu  
35 40 45

Asn Asp Pro Asp Pro Ser Gly Gln Leu Leu Phe Arg Ser Ser Glu Ile  
50 55 60

Leu Trp Asn Leu Leu Glu Lys Ser Ser Lys Glu Glu Val Ile Gln Gln  
65 70 75 80

Leu Ser Asn Leu Glu Cys Leu Leu Ala Leu Lys Glu Val Phe Lys Asn  
85 90 95

Leu Phe Met Arg Gly Phe Ser His Tyr Asp Arg Gln Leu Arg Asn Asp  
100 105 110

Ile Leu Val Ile Thr Thr Ile Ile Ala Gln Asn Pro Glu Ala Pro Met  
115 120 125

Ile Glu Cys Gly Phe Thr Lys Asp Leu Ile Leu Phe Ala Thr Phe Asn  
130 135 140

Glu Val Lys Ser Gln Asn Leu Leu Val Lys Gly Leu Lys Leu Ser Asn  
145 150 155 160

Ser Tyr Glu Asp Phe Glu Leu Lys Lys Leu Leu Phe Asn Val Ile Val  
165 170 175

Ile Leu Cys Lys Asp Leu Pro Thr Val Gln Leu Leu Ile Asp Gly Lys  
180 185 190



Val Ile Leu Ala Leu Phe Thr Tyr Val Lys Lys Pro Glu Lys Gln Lys  
 195 200 205

Ile Ile Asp Trp Ser Ala Ala Gln His Glu Glu Leu Gln Leu His Ala  
 210 215 220

Ile Ala Thr Leu Ser Ser Val Ala Pro Leu Leu Ile Glu Glu Tyr Met  
 225 230 235 240

Ser Cys Gln Gly Asn Ala Arg Val Leu Ala Phe Leu Glu Trp Cys Glu  
 245 250 255

Ser Glu Asp Pro Phe Phe Ser His Gly Asn Ser Phe His Gly Thr Gly  
 260 265 270

Gly Arg Gly Asn Lys Phe Ala Gln Met Arg Tyr Ser Leu Arg Leu Leu  
 275 280 285

Arg Ala Met Val Tyr Leu Glu Asp Glu Thr Val Asn Lys Asp Leu Cys  
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Glu Lys Gly Thr Ile Gln Gln Met Ile Gly Ile Phe Lys Asn Ile Ile  
 305 310 315 320

Ser Lys Pro Asn Glu Lys Glu Glu Ala Ile Val Leu Glu Ile Gln Ser  
 325 330 335

Asp Ile Leu Leu Ile Leu Ser Gly Leu Cys Glu Asn His Ile Gln Arg  
 340 345 350

Lys Glu Ile Phe Gly Thr Glu Gly Val Asp Ile Val Leu His Val Met  
 355 360 365

Lys Thr Asp Pro Arg Lys Leu Gln Ser Gly Leu Gly Tyr Asn Val Leu  
 370 375 380

Leu Phe Ser Thr Leu Asp Ser Ile Trp Cys Cys Ile Leu Gly Cys Tyr  
 385 390 395 400

Pro Ser Glu Asp Tyr Phe Leu Glu Lys Glu Gly Ile Phe Leu Leu Leu  
 405 410 415

Asp Leu Leu Ala Leu Asn Gln Lys Lys Phe Cys Asn Leu Ile Leu Gly  
 420 425 430

Ile Met Val Glu Phe Cys Asp Asn Pro Lys Thr Ala Ala His Val Asn  
435 440 445

Ala Trp Gln Gly Lys Lys Asp Gln Thr Ala Ala Ser Leu Leu Ile Lys  
450 455 460

Leu Trp Arg Lys Glu Glu Lys Glu Leu Gly Val Lys Arg Asp Lys Asn  
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Gly Lys Ile Ile Asp Thr Lys Lys Pro Leu Phe Thr Ser Phe Gln Glu  
485 490 495

Glu Gln Lys Ile Ile Pro Leu Pro Ala Asn Cys Pro Ser Ile Ala Val  
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Met Asp Val Ser Glu Asn Ile Arg Ala Lys Ile Tyr Ala Ile Leu Gly  
515 520 525

Lys Leu Asp Phe Glu Asn Leu Pro Gly Leu Ser Ala Glu Asp Phe Val  
530 535 540

Thr Leu Cys Ile Ile His Arg Tyr Leu Asp Phe Lys Ile Gly Glu Ile  
545 550 555 560

Trp Asn Glu Ile Tyr Glu Glu Ile Lys Leu Glu Lys Leu Arg Pro Val  
565 570 575

Thr Thr Asp Lys Lys Ala Leu Glu Ala Ile Thr Thr Ala Ser Glu Asn  
580 585 590

Ile Gly Lys Met Val Ala Ser Leu Gln Ser Asp Ile Ile Glu Ser Gln  
595 600 605

Ala Cys Gln Asp Met Gln Asn Glu Gln Lys Val Tyr Ala Lys Ile Gln  
610 615 620

Ala Thr His Lys Gln Arg Glu Leu Ala Asn Lys Ser Trp Glu Asp Phe  
625 630 635 640

Leu Ala Arg Thr Ser Asn Ala Lys Thr Leu Lys Lys Ala Lys Arg Leu  
645 650 655

Gln Glu Lys Ala Ile Glu Ala Ser Arg Tyr His Lys Arg Pro Gln Asn  
660 665 670

Ala Ile Phe His Gln Thr His Ile Lys Gly Leu Asn Thr Met Val Pro

675

680

685

Ser Gly Gly Val Val Thr Val Glu Ser Thr Pro Ala Arg Leu Val Gly  
 690 695 700

Gly Pro Leu Val Asp Thr Asp Ile Ala Leu Lys Lys Leu Pro Ile Arg  
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Gly Gly Ala Leu Gln Arg Val Lys Ala Val Lys Ile Val Asp Ala Pro  
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Lys Lys Ser Ile Pro Thr  
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&lt;211&gt; 2727

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<400> 41

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Thr Ile Met Met Lys Ala Gln Ala Ala Ser Gly Ile Cys Thr His Leu
35              40              45

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Asn Asp Pro Asp Pro Ser Gly Gln Leu Leu Phe Arg Ser Ser Glu Ile
50              55              60

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Leu Trp Asn Leu Leu Glu Lys Ser Ser Lys Glu Glu Val Ile Gln Gln
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Leu Ser Asn Leu Glu Cys Leu Leu Ala Leu Lys Glu Val Phe Lys Asn
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Leu Phe Met Arg Gly Phe Ser His Tyr Asp Arg Gln Leu Arg Asn Asp
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Ile Leu Val Ile Thr Thr Ile Ile Ala Gln Asn Pro Glu Ala Pro Met
115             120             125

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Ile Glu Cys Gly Phe Thr Lys Asp Leu Ile Leu Phe Ala Thr Phe Asn
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Glu Val Lys Ser Gln Asn Leu Leu Val Lys Gly Leu Lys Leu Ser Asn  
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Ser Tyr Glu Asp Phe Glu Leu Lys Lys Leu Leu Phe Asn Val Ile Val  
 165 170 175

Ile Leu Cys Lys Asp Leu Pro Thr Val Gln Leu Leu Ile Asp Gly Lys  
 180 185 190

Val Ile Leu Ala Leu Phe Thr Tyr Val Lys Lys Pro Glu Lys Gln Lys  
 195 200 205

Ile Ile Asp Trp Ser Ala Ala Gln His Glu Glu Leu Gln Leu His Ala  
 210 215 220

Ile Ala Thr Leu Ser Ser Val Ala Pro Leu Leu Ile Glu Glu Tyr Met  
 225 230 235 240

Ser Cys Gln Gly Asn Ala Arg Val Leu Ala Phe Leu Glu Trp Cys Glu  
 245 250 255

Ser Glu Asp Pro Phe Phe Ser His Gly Asn Ser Phe His Gly Thr Gly  
 260 265 270

Gly Arg Gly Asn Lys Phe Ala Gln Met Arg Tyr Ser Leu Arg Leu Leu  
 275 280 285

Arg Ala Met Val Tyr Leu Glu Asp Glu Thr Val Asn Lys Asp Leu Cys  
 290 295 300

Glu Lys Gly Thr Ile Gln Gln Met Ile Gly Ile Phe Lys Asn Ile Ile  
 305 310 315 320

Ser Lys Pro Asn Glu Lys Glu Glu Ala Ile Val Leu Glu Ile Gln Ser  
 325 330 335

Asp Ile Leu Leu Ile Leu Ser Gly Leu Cys Glu Asn His Ile Gln Arg  
 340 345 350

Lys Glu Ile Phe Gly Thr Glu Gly Val Asp Ile Val Leu His Val Met  
 355 360 365

Lys Thr Asp Pro Arg Lys Leu Gln Ser Gly Leu Gly Tyr Asn Val Leu  
 370 375 380

Leu Phe Ser Thr Leu Asp Ser Ile Trp Cys Cys Ile Leu Gly Cys Tyr

385		390		395		400
Pro Ser Glu Asp Tyr Phe Leu Glu Lys Glu Gly Ile Phe Leu Leu Leu						
	405			410		415
Asp Leu Leu Ala Leu Asn Gln Lys Lys Phe Cys Asn Leu Ile Leu Gly						
	420			425		430
Ile Met Val Glu Phe Cys Asp Asn Pro Lys Thr Ala Ala His Val Asn						
	435			440		445
Ala Trp Gln Gly Lys Lys Asp Gln Thr Ala Ala Ser Leu Leu Ile Lys						
	450			455		460
Leu Trp Arg Lys Glu Glu Lys Glu Leu Gly Val Lys Arg Asp Lys Asn						
	465			470		475
Gly Lys Ile Ile Asp Phe Glu Asn Leu Pro Gly Leu Ser Ala Glu Asp						
				485		490
Phe Val Thr Leu Cys Ile Ile His Arg Tyr Leu Asp Phe Lys Ile Gln						
	500			505		510
Ala Thr His Lys Gln Arg Glu Leu Ala Asn Lys Ser Trp Glu Asp Phe						
	515			520		525
Leu Ala Arg Thr Ser Asn Ala Lys Thr Leu Lys Lys Ala Lys Arg Leu						
	530			535		540
Gln Glu Lys Ala Ile Glu Ala Ser Arg Tyr His Lys Arg Pro Gln Asn						
	545			550		555
Ala Ile Phe His Gln Thr His Ile Lys Gly Leu Asn Thr Met Val Pro						
				565		570
Ser Gly Gly Val Val Thr Val Glu Ser Thr Pro Ala Arg Leu Val Gly						
	580			585		590
Gly Pro Leu Val Asp Thr Asp Ile Ala Leu Lys Lys Leu Pro Ile Arg						
	595			600		605
Gly Gly Ala Leu Gln Arg Val Lys Ala Val Lys Ile Val Asp Ala Pro						
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Lys Lys Ser Ile Pro Thr						
	625					630

<210> 42  
 <211> 2820  
 <212> DNA  
 <213> Artificial

<220>

<223> cDNA or putative protein derived from a cDNA.

<400> 42

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cagccagtgg	aatctgtact	cacctcaatg	accagatcc	ctctggacag	cttttatttc	180
gttcatcaga	aatacttttg	aacttgctgg	aaaaatcttc	aaaagaagaa	gtcatataac	240
agcttagtaa	cttggaaatg	ttgctggctt	tgaagggaat	atttaaaaat	ctgtttatga	300
gaggtttcag	tcattatgac	cgtcagctta	gaaatgacat	attagtgatc	actacaatta	360
tagctcaaaa	tcctgaagca	ccaatgattg	aatgtggctt	taccaaggat	ttgatactgt	420
ttgccacctt	taatgaagtt	aaaagtcaaa	atcttttgg	aaaaggactt	aagcttttcta	480
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cgtttttcag	tcattggaac	agttttcatg	gtacaggtgg	ccgaggcaac	aagtttgccc	840
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catccaaaac	atatggatag	agtggggaat	cagggtacta	ttatcagaag	caagtatata	2640
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ttatgttttc	tctgctataa	aagcaaatgt	tagtcatgag	ccaaatggta	aaaagaaaa	2760
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<210> 43  
 <211> 661

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; cDNA or putative protein derived from a cDNA.

&lt;400&gt; 43

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Trp Val Leu Lys Val Leu Gln His Leu Ser Thr Ser Glu Val Asn Cys  
20 25 30

Thr Ile Met Met Lys Ala Gln Ala Ala Ser Gly Ile Cys Thr His Leu  
35 40 45

Asn Asp Pro Asp Pro Ser Gly Gln Leu Leu Phe Arg Ser Ser Glu Ile  
50 55 60

Leu Trp Asn Leu Leu Glu Lys Ser Ser Lys Glu Glu Val Ile Gln Gln  
65 70 75 80

Leu Ser Asn Leu Glu Cys Leu Leu Ala Leu Lys Glu Val Phe Lys Asn  
85 90 95

Leu Phe Met Arg Gly Phe Ser His Tyr Asp Arg Gln Leu Arg Asn Asp  
100 105 110

Ile Leu Val Ile Thr Thr Ile Ile Ala Gln Asn Pro Glu Ala Pro Met  
115 120 125

Ile Glu Cys Gly Phe Thr Lys Asp Leu Ile Leu Phe Ala Thr Phe Asn  
130 135 140

Glu Val Lys Ser Gln Asn Leu Leu Val Lys Gly Leu Lys Leu Ser Asn  
145 150 155 160

Ser Tyr Glu Asp Phe Glu Leu Lys Lys Leu Leu Phe Asn Val Ile Val  
165 170 175

Ile Leu Cys Lys Asp Leu Pro Thr Val Gln Leu Leu Ile Asp Gly Lys  
180 185 190

Val Ile Leu Ala Leu Phe Thr Tyr Val Lys Lys Pro Glu Lys Gln Lys  
195 200 205

Ile Ile Asp Trp Ser Ala Ala Gln His Glu Glu Leu Gln Leu His Ala



210	215	220	
Ile Ala Thr Leu Ser Ser Val Ala Pro Leu Leu Ile Glu Glu Tyr Met			
225	230	235	240
Ser Cys Gln Gly Asn Ala Arg Val Leu Ala Phe Leu Glu Trp Cys Glu			
	245	250	255
Ser Glu Asp Pro Phe Phe Ser His Gly Asn Ser Phe His Gly Thr Gly			
	260	265	270
Gly Arg Gly Asn Lys Phe Ala Gln Met Arg Tyr Ser Leu Arg Leu Leu			
	275	280	285
Arg Ala Met Val Tyr Leu Glu Asp Glu Thr Val Asn Lys Asp Leu Cys			
	290	295	300
Glu Lys Gly Thr Ile Gln Gln Met Ile Gly Ile Phe Lys Asn Ile Ile			
305	310	315	320
Ser Lys Pro Asn Glu Lys Glu Glu Ala Ile Val Leu Glu Ile Gln Ser			
	325	330	335
Asp Ile Leu Leu Ile Leu Ser Gly Leu Cys Glu Asn His Ile Gln Arg			
	340	345	350
Lys Glu Ile Phe Gly Thr Glu Gly Val Asp Ile Val Leu His Val Met			
	355	360	365
Lys Thr Asp Pro Arg Lys Leu Gln Ser Gly Leu Gly Tyr Asn Val Leu			
	370	375	380
Leu Phe Ser Thr Leu Asp Ser Ile Trp Cys Cys Ile Leu Gly Cys Tyr			
385	390	395	400
Pro Ser Glu Asp Tyr Phe Leu Glu Lys Glu Gly Ile Phe Leu Leu Leu			
	405	410	415
Asp Leu Leu Ala Leu Asn Gln Lys Lys Phe Cys Asn Leu Ile Leu Gly			
	420	425	430
Ile Met Val Glu Phe Cys Asp Asn Pro Lys Thr Ala Ala His Val Asn			
	435	440	445
Ala Trp Gln Gly Lys Lys Asp Gln Thr Ala Ala Ser Leu Leu Ile Lys			
450	455	460	

Leu Trp Arg Lys Glu Glu Lys Glu Leu Gly Val Lys Arg Asp Lys Asn  
 465 470 475 480

Gly Lys Ile Ile Asp Phe Glu Asn Leu Pro Gly Leu Ser Ala Glu Asp  
 485 490 495

Phe Val Thr Leu Cys Ile Ile His Arg Tyr Leu Asp Phe Lys Ile Gly  
 500 505 510

Glu Ile Trp Asn Glu Ile Tyr Glu Glu Ile Lys Leu Glu Lys Leu Arg  
 515 520 525

Pro Val Thr Thr Asp Lys Lys Ala Leu Glu Ala Ile Thr Thr Ala Ser  
 530 535 540

Glu Asn Ile Gly Lys Met Val Ala Ser Leu Gln Ser Asp Ile Ile Glu  
 545 550 555 560

Ser Gln Ala Cys Gln Asp Met Gln Asn Glu Gln Lys Val Tyr Ala Lys  
 565 570 575

Ile Gln Ala Thr His Lys Gln Arg Glu Leu Ala Asn Lys Ser Trp Glu  
 580 585 590

Asp Phe Leu Ala Arg Thr Ser Asn Ala Lys Thr Leu Lys Val Pro Ser  
 595 600 605

Gly Gly Val Val Thr Val Glu Ser Thr Pro Ala Arg Leu Val Gly Gly  
 610 615 620

Pro Leu Val Asp Thr Asp Ile Ala Leu Lys Lys Leu Pro Ile Arg Gly  
 625 630 635 640

Gly Ala Leu Gln Arg Val Lys Ala Val Lys Ile Val Asp Ala Pro Lys  
 645 650 655

Lys Ser Ile Pro Thr  
 660

<210> 44

<211> 565

<212> DNA

<213> Artificial

<220>

<223> cDNA or putative protein derived from a cDNA.

<400> 44  
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 aatttagata ggtatcaagc tgtaactaag acaatatttg ataaatgttg gatgacattt 180  
 aatttaattg agcatgtact tatttgcatt tgctggcagt tcaggcatag ttaaagttag 240  
 agttctccta tatttcataa taagtgggtc tgccaaaacc catgtattaa ataaattgtc 300  
 caagtgaaac tcgactaact ttggcctttg tgtatttcct gaaggtaata ttgttaactg 360  
 ttaataaata cttctgacac tacattttaa tgtttgcaga ttctgcaaac taattgctca 420  
 ttgtaatgtt gaaataattt ggatatttca cattgaaatg aaaagccttt ctctggagca 480  
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 gtattataaa actcagataa aagac 565

<210> 45

<211> 3471

<212> DNA

<213> Artificial

<220>

<223> cDNA or putative protein derived from a cDNA.

<400> 45  
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 cccgtctccc tccctccctct cggacagctc ttcttccttc ggcaaaggct tccacccctg 240  
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 ggcagcagcc gcggtcgcg cggccctggt gtccgactcg ttcagctgag cggcgtcctc 420  
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 cgcgggctg cagggcactt acccgcggtt gggcatggcg cacccgtaag agtcgtgggt 540  
 taagccctcg caccggggcc tgggtgctgc gggcgagggt ggctcggccg gcgcctccag 600  
 ctggtgggac gtgggggccc gctggatcga cgtgcagaac ccgaacagcg cggctgcgct 660  
 gcccggtcgt ctgcacctg ccgcccgggg gctccaaacc tcgctgact cgcgcctcgg 720  
 aggctacaac tcggattact cgggcctgag tcaactcgcc ttcagcagcg gcgcctcctc 780  
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 gatgcaagtt tcagcaaagg gcagtcttgt cgaatcgctg cagcagcttt ctttcatctt 2220  
 tatagcatat attttatttt taaaaaaact aggggaaaaa tagcaacctt ccatttggtt 2280

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<210> 46  
 <211> 452  
 <212> PRT  
 <213> Artificial

<220>  
 <223> cDNA or putative protein derived from a cDNA.

<400> 46

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Leu Ala Met Leu Ala Ala Thr Cys Asn Lys Ile Gly Ser Pro Ser Pro
20           25           30

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Ser Pro Ser Ser Leu Ser Asp Ser Ser Ser Ser Phe Gly Lys Gly Phe
35           40           45

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His Pro Trp Lys Arg Ser Ser Ser Ser Ser Ser Ala Ser Cys Asn Val
50           55           60

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Val Gly Ser Ser Leu Ser Ser Phe Gly Val Ser Gly Ala Ser Arg Asn
65           70           75           80

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Gly Gly Ser Ser Ser Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
85           90           95

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Ala Ala Ala Leu Val Ser Asp Ser Phe Ser Cys Gly Gly Ser Ser Ala
100          105          110

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His Ser Gln Asp Gly Ser His Gln Pro Val Phe Ile Ser Lys Val His

115	120	125
Thr Ser Val Asp Gly Leu Gln Gly Ile Tyr Pro Arg Val Gly Met Ala 130 135 140		
His Pro Tyr Glu Ser Trp Phe Lys Pro Ser His Pro Gly Leu Gly Ala 145 150 155 160		
Ala Gly Glu Val Gly Ser Ala Gly Ala Ser Ser Trp Trp Asp Val Gly 165 170 175		
Ala Gly Trp Ile Asp Val Gln Asn Pro Asn Ser Ala Ala Ala Leu Pro 180 185 190		
Gly Ser Leu His Pro Ala Ala Gly Gly Leu Gln Thr Ser Leu His Ser 195 200 205		
Pro Leu Gly Gly Tyr Asn Ser Asp Tyr Ser Gly Leu Ser His Ser Ala 210 215 220		
Phe Ser Ser Gly Ala Ser Ser His Leu Leu Ser Pro Ala Gly Gln His 225 230 235 240		
Leu Met Asp Gly Phe Lys Pro Val Leu Pro Gly Ser Tyr Pro Asp Ser 245 250 255		
Ala Pro Ser Pro Leu Ala Gly Ala Gly Gly Ser Met Leu Ser Ala Gly 260 265 270		
Pro Ser Ala Pro Leu Gly Gly Ser Pro Arg Ser Ser Ala Arg Arg Tyr 275 280 285		
Ser Gly Arg Ala Thr Cys Asp Cys Pro Asn Cys Gln Glu Ala Glu Arg 290 295 300		
Leu Gly Pro Ala Gly Ala Ser Leu Arg Arg Lys Gly Leu His Ser Cys 305 310 315 320		
His Ile Pro Gly Cys Gly Lys Val Tyr Gly Lys Thr Ser His Leu Lys 325 330 335		
Ala His Leu Arg Trp His Thr Gly Glu Arg Pro Phe Val Cys Asn Trp 340 345 350		
Leu Phe Cys Gly Lys Arg Phe Thr Arg Ser Asp Glu Leu Gln Arg His 355 360 365		

Leu Arg Thr His Thr Gly Glu Lys Arg Phe Ala Cys Pro Val Cys Asn  
 370 375 380

Lys Arg Phe Met Arg Ser Asp His Leu Ser Lys His Val Lys Thr His  
 385 390 395 400

Ser Gly Gly Gly Gly Gly Gly Gly Ser Ala Gly Ser Gly Ser Gly Gly  
 405 410 415

Lys Lys Gly Ser Asp Thr Asp Ser Glu His Ser Ala Ala Gly Ser Pro  
 420 425 430

Pro Cys His Ser Pro Glu Leu Leu Gln Pro Pro Glu Pro Gly His Arg  
 435 440 445

Asn Gly Leu Glu  
 450

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 <211> 501  
 <212> DNA  
 <213> Artificial

<220>  
 <223> cDNA or putative protein derived from a cDNA.

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 cccgcttaac tgcagcta atcaaaagca ctggtatggg ctgtctatct gtgctggaac 180  
 ctgagtttat ctttgtctgc aattacgatt cttctgggtt tattttgcca gctcattatc 240  
 cagccccctg gaatcaggcc tcccaaattt agcagggtgct ggggaggacc ctaggaggatg 300  
 gggttatggg ggctagctgg tgaaactgcc ctttccttct tgttctatga gtgtgatggg 360  
 gtttgagaaa atgtggggct atggttcagg cgacttcac atgtgcaaag atggagaaag 420  
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 aaatggttatt tttaaagtta a 501

<210> 48  
 <211> 3135  
 <212> DNA  
 <213> Artificial

<220>  
 <223> cDNA or putative protein derived from a cDNA.

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 tagggcggag ctgttgggtg gaccgagcag gcgaggcgca ggcaggcagc ggctccgcct 180  
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 cctgtttcct cgacccccag cactcctcca ggcctagttc gcttcagagg cgcgagaccc 300  
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&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; cDNA or putative protein derived from a cDNA.

&lt;400&gt; 49

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Phe Pro Leu Thr His Thr Arg Arg Leu Glu Glu Glu Ala Ala Leu Asp  
35 40 45

Thr Pro Val Ala Pro Leu Pro Gly Gly Ala Gln Pro Gly Ala Leu Ala  
50 55 60

Ala Ala Leu Gly Ala Gly Pro Arg Arg Leu Gly Leu Gly Thr Gln Gly  
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&lt;210&gt; 53

&lt;211&gt; 95

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&lt;223&gt; cDNA or putative protein derived from a cDNA.

&lt;400&gt; 53

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Pro Val Ala Pro Leu Pro Gly Gly Ala Gln Pro Gly Ala Leu Ala Ala
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Ala Leu Gly Ala Gly Pro Arg Arg Leu Gly Leu Gly Thr Gln Gly Trp
50             55             60

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Ala Arg Arg Arg Arg Trp Ala Gln Gly Ser Pro Glu Asn Pro His Glu
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Leu Thr Arg Arg Ala Ala Gly Pro Val Gly Thr Gly Pro Pro Arg
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&lt;220&gt;

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&lt;400&gt; 54

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20 25 30

Val Ser Pro Ile Phe Pro Phe Ser Pro Arg Ser Pro Phe Gln Pro Leu  
35 40 45

Ile Pro Arg Thr Pro Gly Ser Pro Trp Gly Pro Val Gly Pro Ala Ser  
50 55 60

Pro Leu Gly Pro Gly Phe Pro Ile Gly Pro Met Gly Pro Gly Lys Pro  
65 70 75 80

Val Gly Pro Lys Gly Pro Met Leu Pro Leu Gly Pro Ser Gly Pro Val  
 . 85 90 95

Gly Pro Thr Ser Pro Leu Phe Pro Phe Cys Pro  
100 105

<210>	56
<211>	1439
<212>	DNA
<213>	Artificial

<223> cDNA or putative protein derived from a cDNA.

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<400> 56
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gggcaggaca gcttgagat agggcccgga attgcgggcg tcaactctgct cctgcgacct 120

```

```

agccaggcgt gagggagtga cagcagcgca ttgcggggac gagagcgatg agtgagaacg 180
ccgcaccagg tctgatctca gagctgaagc tggctgtgcc ctggggccac atcgagcca 240
aagcctgggg ctccctgcag ggccctccag ttctctgcct gcacggctgg ctggacaatg 300
ccagctcctt cgacagactc atccctcttc tcccgcaaga cttttattac gttgccatgg 360
atttcggagg tcatgggctc tcgtcccatt acagcccagg tgtcccatat tacctccaga 420
cttttgtgag tgagatccga agagttgtgg cagccttgaa atggaatcga ttctccattc 480
tggggccacag cttcggtggc gtcgtgggag gaatgttttt ctgtaccttc cccgagatgg 540
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```

&lt;210&gt; 57

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; cDNA or putative protein derived from a cDNA.

&lt;400&gt; 57

```

Met Ser Glu Asn Ala Ala Pro Gly Leu Ile Ser Glu Leu Lys Leu Ala
1           5           10           15

```

```

Val Pro Trp Gly His Ile Ala Ala Lys Ala Trp Gly Ser Leu Gln Gly
20           25           30

```

```

Pro Pro Val Leu Cys Leu His Gly Trp Leu Asp Asn Ala Ser Ser Phe
35           40           45

```

```

Asp Arg Leu Ile Pro Leu Leu Pro Gln Asp Phe Tyr Tyr Val Ala Met
50           55           60

```

```

Asp Phe Gly Gly His Gly Leu Ser Ser His Tyr Ser Pro Gly Val Pro
65           70           75           80

```

```

Tyr Tyr Leu Gln Thr Phe Val Ser Glu Ile Arg Arg Val Val Ala Ala
85           90           95

```

```

Leu Lys Trp Asn Arg Phe Ser Ile Leu Gly His Ser Phe Gly Gly Val
100          105          110

```

Val Gly Gly Met Phe Phe Cys Thr Phe Pro Glu Met Val Asp Lys Leu  
 115 120 125

Ile Leu Leu Asp Thr Pro Leu Phe Leu Leu Glu Ser Asp Glu Met Glu  
 130 135 140

Asn Leu Leu Thr Tyr Lys Arg Arg Ala Ile Glu His Val Leu Gln Val  
 145 150 155 160

Glu Ala Ser Gln Glu Pro Ser His Val Phe Ser Leu Lys Gln Leu Leu  
 165 170 175

Gln Arg Leu Leu Lys Ser Asn Ser His Leu Ser Glu Glu Cys Gly Glu  
 180 185 190

Leu Leu Leu Gln Arg Gly Thr Thr Lys Val Ala Thr Gly Leu Val Leu  
 195 200 205

Asn Arg Asp Gln Arg Leu Ala Trp Ala Glu Asn Ser Ile Asp Phe Ile  
 210 215 220

Ser Arg Glu Leu Cys Ala His Ser Ile Arg Lys Leu Gln Ala His Val  
 225 230 235 240

Leu Leu Ile Lys Ala Val His Gly Tyr Phe Asp Ser Arg Gln Asn Tyr  
 245 250 255

Ser Glu Lys Glu Ser Leu Ser Phe Met Ile Asp Thr Met Lys Ser Thr  
 260 265 270

Leu Lys Glu Gln Phe Gln Phe Val Glu Val Pro Gly Asn His Cys Val  
 275 280 285

His Met Ser Glu Pro Gln His Val Ala Ser Ile Ile Ser Ser Phe Leu  
 290 295 300

Gln Cys Thr His Met Leu Pro Ala Gln Leu  
 305 310

<210> 58

<211> 1280

<212> DNA

<213> Artificial

<220>

<223> cDNA or putative protein derived from a cDNA.

<400> 58

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agccaggcgt gaggagtgag cagcagcgca ttcgcgggac gagagcgatg agtgagaacg      180
ccgcaccagg tctgatctca gagctgaagc tggctgtgcc ctggggccac atcgagcca      240
aagcctgggg ctccctgcag ggcctccag ttctctgcct gcacggctgg ctggacaatg      300
ccagctcctt cgacagactc atccctcttc tcccgcaaga cttttattac gttgccatgg      360
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caggcccatg tcctgttgat caagtaagtc tggacccatc cccttcagcc acccgccaag      900
gagacatggg cgccaggaat ctccgggagg gggccctggc atgaggctcc aagttctctg      960
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<210> 59  
 <211> 209  
 <212> PRT  
 <213> Artificial

<220>  
 <223> cDNA or putative protein derived from a cDNA.  
 <400> 59

Met Ser Glu Asn Ala Ala Pro Gly Leu Ile Ser Glu Leu Lys Leu Ala  
 1 5 10 15

Val Pro Trp Gly His Ile Ala Ala Lys Ala Trp Gly Ser Leu Gln Gly  
 20 25 30

Pro Pro Val Leu Cys Leu His Gly Trp Leu Asp Asn Ala Ser Ser Phe  
 35 40 45

Asp Arg Leu Ile Pro Leu Leu Pro Gln Asp Phe Tyr Tyr Val Ala Met  
 50 55 60

Asp Phe Gly Gly His Gly Leu Ser Ser His Tyr Ser Pro Gly Val Pro  
 65 70 75 80

Tyr Tyr Leu Gln Thr Phe Val Ser Glu Ile Arg Arg Val Val Ala Ala  
 85 90 95

Leu Lys Trp Asn Arg Phe Ser Ile Leu Gly His Ser Phe Gly Gly Val  
 100 105 110

Val Gly Gly Met Phe Phe Cys Thr Phe Pro Glu Met Val Asp Lys Leu  
 115 120 125

Ile Leu Leu Asp Thr Pro Leu Phe Leu Leu Glu Ser Asp Glu Met Glu  
 130 135 140

Asn Leu Leu Thr Tyr Lys Arg Arg Ala Ile Glu His Val Leu Gln Val  
 145 150 155 160

Glu Ala Ser Gln Glu Pro Ser His Val Phe Ser Leu Lys Gln Leu Leu  
 165 170 175

Gln Arg Leu Leu Lys Ser Asn Ser His Leu Ser Glu Glu Cys Gly Glu  
 180 185 190

Leu Leu Leu Gln Arg Gly Thr Thr Lys Val Ala Thr Gly Arg Glu Gln  
 195 200 205

His

<210> 60

<211> 1957

<212> DNA

<213> Artificial

<220>

<223> cDNA or putative protein derived from a cDNA.

<400> 60

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```

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&lt;210&gt; 61

&lt;211&gt; 244

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; cDNA or putative protein derived from a cDNA.

&lt;400&gt; 61

```

Met Phe Arg Gly Thr Pro Gly Ser Pro Gly Lys Gly Gly Ser Val Leu
1           5           10           15

```

```

Ser Phe Phe Pro Leu Phe Ile Leu Pro Phe Trp His Pro His Met Phe
          20           25           30

```

```

Phe Cys Thr Phe Pro Glu Met Val Asp Lys Leu Ile Leu Leu Asp Thr
          35           40           45

```

```

Pro Leu Phe Leu Leu Glu Ser Asp Glu Met Glu Asn Leu Leu Thr Tyr
          50           55           60

```

```

Lys Arg Arg Ala Ile Glu His Val Leu Gln Val Glu Ala Ser Gln Glu
65           70           75           80

```

```

Pro Ser His Val Phe Ser Leu Lys Gln Leu Leu Gln Arg Leu Leu Lys
          85           90           95

```

```

Ser Asn Ser His Leu Ser Glu Glu Cys Gly Glu Leu Leu Leu Gln Arg
          100          105          110

```

```

Gly Thr Thr Lys Val Ala Thr Gly Leu Val Leu Asn Arg Asp Gln Arg
          115          120          125

```

```

Leu Ala Trp Ala Glu Asn Ser Ile Asp Phe Ile Ser Arg Glu Leu Cys
          130          135          140

```

```

Ala His Ser Ile Arg Lys Leu Gln Ala His Val Leu Leu Ile Lys Ala
145          150          155          160

```

Val His Gly Tyr Phe Asp Ser Arg Gln Asn Tyr Ser Glu Lys Glu Ser  
 165 170 175

Leu Ser Phe Met Ile Asp Thr Met Lys Ser Thr Leu Lys Glu Val Arg  
 180 185 190

Arg Gly Ser Gly Ser Trp Cys Pro Ala Thr Val Ala His Ser Gly Pro  
 195 200 205

Thr Ser Pro Ile Ser Ser His Ala Leu Gly Arg Pro Trp Val Cys Pro  
 210 215 220

Gln Ala Gln Gln Val Thr Thr Arg Ile Tyr Gln Ala Ser Cys Ser Thr  
 225 230 235 240

Val Val Ser Pro

<210> 62  
 <211> 1165  
 <212> DNA  
 <213> Artificial

<220>  
 <223> cDNA or putative protein derived from a cDNA.

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 aatggaatcg attctccatt ctgggccaca gcttcggtgg cgtcgtgggc ggaatgtttt 420  
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<210> 63  
 <211> 351  
 <212> PRT  
 <213> Artificial

<220>

<223> cDNA or putative protein derived from a cDNA.

<400> 63

Lys Asn Ile Leu Ala Arg Gly Trp Arg Thr Glu Ala Gly Ala Arg Gly  
1 5 10 15

Glu Gly Gly Gln Pro Ser Arg Arg Ala Tyr Asn Ser Pro Gly Leu Ile  
20 25 30

Ser Glu Leu Lys Leu Ala Val Pro Trp Gly His Ile Ala Ala Lys Ala  
35 40 45

Trp Gly Ser Leu Gln Gly Pro Pro Val Leu Cys Leu His Gly Trp Leu  
50 55 60

Asp Asn Ala Ser Ser Phe Asp Arg Leu Ile Pro Leu Leu Pro Gln Asp  
65 70 75 80

Phe Tyr Tyr Val Ala Met Asp Phe Gly Gly His Gly Leu Ser Ser His  
85 90 95

Tyr Ser Pro Gly Val Pro Tyr Tyr Leu Gln Thr Phe Val Ser Glu Ile  
100 105 110

Arg Arg Val Val Ala Ala Leu Lys Trp Asn Arg Phe Ser Ile Leu Gly  
115 120 125

His Ser Phe Gly Gly Val Val Gly Gly Met Phe Phe Cys Thr Phe Pro  
130 135 140

Glu Met Val Asp Lys Leu Ile Leu Leu Asp Thr Pro Leu Phe Leu Leu  
145 150 155 160

Glu Ser Asp Glu Met Glu Asn Leu Leu Thr Tyr Lys Arg Arg Ala Ile  
165 170 175

Glu His Val Leu Gln Val Glu Ala Ser Gln Glu Pro Ser His Val Phe  
180 185 190

Ser Leu Lys Gln Leu Leu Gln Arg Leu Leu Lys Ser Asn Ser His Leu  
195 200 205

Ser Glu Glu Cys Gly Glu Leu Leu Leu Gln Arg Gly Thr Thr Lys Val  
210 215 220

Ala Thr Gly Leu Val Leu Asn Arg Asp Gln Arg Leu Ala Trp Ala Glu

225                                      230                                      235                                      240  
 Asn Ser Ile Asp Phe Ile Ser Arg Glu Leu Cys Ala His Ser Ile Arg  
    245                                      250                                      255  
 Lys Leu Gln Ala His Val Leu Leu Ile Lys Ala Val His Gly Tyr Phe  
    260                                      265                                      270  
 Asp Ser Arg Gln Asn Tyr Ser Glu Lys Glu Ser Leu Ser Phe Met Ile  
    275                                      280                                      285  
 Asp Thr Met Lys Ser Thr Leu Lys Glu Val Arg Arg Gly Ser Gly Ser  
    290                                      295                                      300  
 Trp Cys Pro Ala Thr Val Ala His Ser Gly Pro Thr Ser Pro Ile Ser  
 305                                      310                                      315                                      320  
 Ser His Ala Leu Gly Arg Pro Trp Val Cys Pro Gln Ala Gln Gln Val  
    325                                      330                                      335  
 Thr Thr Arg Ile Tyr Gln Ala Ser Cys Ser Thr Val Val Ser Pro  
    340                                      345                                      350

&lt;210&gt; 64

&lt;211&gt; 2258

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; cDNA or putative protein derived from a cDNA.

&lt;400&gt; 64

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&lt;210&gt; 65

&lt;211&gt; 3329

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; cDNA or putative protein derived from a cDNA.

&lt;400&gt; 65

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&lt;210&gt; 66

&lt;211&gt; 601

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; cDNA or putative protein derived from a cDNA.

&lt;400&gt; 66

Met	Pro	Glu	Arg	Glu	Leu	Trp	Pro	Ala	Gly	Thr	Gly	Ser	Glu	Pro	Val
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Thr	Arg	Val	Gly	Ser	Cys	Asp	Ser	Met	Met	Ser	Ser	Thr	Ser	Thr	Arg
		20						25					30		

Ser	Gly	Ser	Ser	Asp	Ser	Ser	Tyr	Asp	Phe	Leu	Ser	Thr	Glu	Glu	Lys
	35						40					45			

Glu	Cys	Leu	Leu	Phe	Leu	Glu	Glu	Thr	Ile	Gly	Ser	Leu	Asp	Thr	Glu
	50				55					60					

Ala	Asp	Ser	Gly	Leu	Ser	Thr	Asp	Glu	Ser	Glu	Pro	Ala	Thr	Thr	Pro
65				70					75						80

Arg	Gly	Phe	Arg	Ala	Leu	Pro	Ile	Thr	Gln	Pro	Thr	Pro	Arg	Gly	Gly
			85					90						95	

Pro	Glu	Glu	Thr	Ile	Thr	Gln	Gln	Gly	Arg	Thr	Pro	Arg	Thr	Val	Thr
			100					105					110		

Glu Ser Ser Ser Ser His Pro Pro Glu Pro Gln Gly Leu Gly Leu Arg  
 115 120 125

Ser Gly Ser Tyr Ser Leu Pro Arg Asn Ile His Ile Ala Arg Ser Gln  
 130 135 140

Asn Phe Arg Lys Ser Thr Thr Gln Ala Ser Ser His Asn Pro Gly Glu  
 145 150 155 160

Pro Gly Arg Leu Ala Pro Glu Pro Glu Lys Glu Gln Val Ser Gln Ser  
 165 170 175

Ser Gln Pro Arg Gln Ala Pro Ala Ser Pro Gln Glu Ala Ala Leu Asp  
 180 185 190

Leu Asp Val Val Leu Ile Pro Pro Pro Glu Ala Phe Arg Asp Thr Gln  
 195 200 205

Pro Glu Gln Cys Arg Glu Ala Ser Leu Pro Glu Gly Pro Gly Gln Gln  
 210 215 220

Gly His Thr Pro Gln Leu His Thr Pro Ser Ser Ser Gln Glu Arg Glu  
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Gln Thr Pro Ser Glu Ala Met Ser Gln Lys Ala Lys Glu Thr Val Ser  
 245 250 255

Thr Arg Tyr Thr Gln Pro Gln Pro Pro Pro Ala Gly Leu Pro Gln Asn  
 260 265 270

Ala Arg Ala Glu Asp Ala Pro Leu Ser Ser Gly Glu Asp Pro Asn Ser  
 275 280 285

Arg Leu Ala Pro Leu Thr Thr Pro Lys Pro Arg Lys Leu Pro Pro Asn  
 290 295 300

Ile Val Leu Lys Ser Ser Arg Ser Ser Phe His Ser Asp Pro Gln His  
 305 310 315 320

Trp Leu Ser Arg His Thr Glu Ala Ala Pro Gly Asp Ser Gly Leu Ile  
 325 330 335

Ser Cys Ser Leu Gln Glu Gln Arg Lys Ala Arg Lys Glu Ala Leu Glu  
 340 345 350

Lys Leu Gly Leu Pro Gln Asp Gln Asp Glu Pro Gly Leu His Leu Ser  
 355 360 365

Lys Pro Thr Ser Ser Ile Arg Pro Lys Glu Thr Arg Ala Gln His Leu  
 370 375 380

Ser Pro Ala Pro Gly Leu Ala Gln Pro Ala Ala Pro Ala Gln Ala Ser  
 385 390 395 400

Ala Ala Ile Pro Ala Ala Gly Lys Ala Leu Ala Gln Ala Pro Ala Pro  
 405 410 415

Ala Pro Gly Pro Ala Gln Gly Pro Leu Pro Met Lys Ser Pro Ala Pro  
 420 425 430

Gly Asn Val Ala Ala Ser Lys Ser Met Pro Ile Pro Ile Pro Lys Ala  
 435 440 445

Pro Arg Ala Asn Ser Ala Leu Thr Pro Pro Lys Pro Glu Ser Gly Leu  
 450 455 460

Thr Leu Gln Glu Ser Asn Thr Pro Gly Leu Arg Gln Met Asn Phe Lys  
 465 470 475 480

Ser Asn Thr Leu Glu Arg Ser Gly Val Gly Leu Ser Ser Tyr Leu Ser  
 485 490 495

Thr Glu Lys Asp Ala Ser Pro Lys Thr Ser Thr Ser Leu Gly Lys Gly  
 500 505 510

Ser Phe Leu Asp Lys Ile Ser Pro Ser Val Leu Arg Asn Ser Arg Pro  
 515 520 525

Arg Pro Ala Ser Leu Gly Thr Gly Lys Asp Phe Ala Gly Ile Gln Val  
 530 535 540

Gly Lys Leu Ala Asp Leu Glu Gln Glu Gln Ser Ser Lys Arg Leu Ser  
 545 550 555 560

Tyr Gln Gly Gln Ser Arg Asp Lys Leu Pro Arg Pro Pro Cys Val Ser  
 565 570 575

Val Lys Ile Ser Pro Lys Gly Val Pro Asn Glu His Arg Arg Glu Ala  
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Leu Lys Lys Leu Gly Leu Leu Lys Glu  
595 600

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<211> 753  
<212> DNA  
<213> Artificial

<220>  
<223> cDNA or putative protein derived from a cDNA.

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cgaagagttg tggcagggtg cgtcgtgggc ggaatgtttt tctgtacctt ccccgagatg 180  
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gagccctcgc acgtgttcag cctgaagcag ctgctgcaga ggttactgaa gagcaatagc 360  
cacttgagtg aggagtgcgg ggagcttctc ctgcaaagag gaaccacgaa ggtggccaca 420  
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<211> 2561  
<212> DNA  
<213> Artificial

<220>  
<223> cDNA or putative protein derived from a cDNA.

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&lt;210&gt; 69

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; cDNA or putative protein derived from a cDNA.

&lt;400&gt; 69

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Met Lys Val Glu Pro Trp Arg Ala Gly Pro Gly Arg Arg Ala Trp Ser
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```

Glu Gly Ala Gly Gln Ala Pro Gln Lys Arg Ala Arg Ala Gly Ala Glu
20           25           30

```

```

Pro Gln Leu Pro Ala Thr Pro Ala Leu Pro Gly Gly Lys Met Val Ala
35           40           45

```

```

Arg Arg Arg Lys Cys Ala Arg Gly Thr Arg Arg Pro Tyr Pro Glu Pro
50           55           60

```

```

Thr Ala Tyr Ala Ala Ile Pro Ile Lys Phe Ser Glu Lys Gln Gln Ala
65           70           75           80

```

```

Ser His Tyr Leu Tyr Val Arg Ala His Gly Val Arg Gln Gly Thr Lys
85           90           95

```

```

Ser Thr Trp Pro Gln Lys Arg Thr Leu Phe Val Leu Asn Val Pro Pro
100          105          110

```

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Tyr Cys Thr Glu Glu Ser Leu Ser Arg Leu Leu Ser Thr Cys Gly Leu
115          120          125

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Val Gln Ser Val Glu Leu Gln Glu Lys Pro Asp Leu Ala Glu Ser Pro  
 130 135 140

Lys Glu Ser Arg Ser Lys Phe Phe His Pro Lys Pro Val Pro Gly Phe  
 145 150 155 160

Gln Val Ala Tyr Val Val Phe Gln Lys Pro Ser Gly Val Ser Ala Ala  
 165 170 175

Leu Ala Leu Lys Gly Pro Leu Leu Val Ser Thr Glu Ser His Pro Val  
 180 185 190

Lys Ser Gly Ile His Lys Trp Ile Ser Asp Tyr Ala Asp Ser Val Pro  
 195 200 205

Asp Pro Glu Ala Leu Arg Val Glu Val Asp Thr Phe Met Glu Ala Tyr  
 210 215 220

Asp Gln Lys Ile Ala Glu Glu Glu Ala Lys Ala Lys Gly Glu Glu Gly  
 225 230 235 240

Val Pro Asp Glu Glu Gly Trp Val Lys Val Thr Arg Arg Gly Arg Arg  
 245 250 255

Leu Cys Ser Pro Gly Leu Arg Gln Pro Ala Cys Gly Cys Trp Arg Gly  
 260 265 270

Arg Asp Gly Ser Ala Ala Lys Arg Ala Ala Gln Leu Leu Arg Leu Ala  
 275 280 285

Ala Ser Arg Glu Gln Asp Gly Ala Ser Ser Ala Ala Arg Lys Lys Phe  
 290 295 300

Glu Glu Asp Lys Gln Arg Ile Glu Leu Leu Arg Ala Gln Arg Lys Phe  
 305 310 315 320

Arg Pro Tyr